

1 / 4 9

SEQUENCE LISTING

<110> National Agricultural Research Organization

<120> JUVENILE HORMONE TRANSMETHYLASE GENES
AND METHOD OF USING THE SAME

<130> ARO-A0301P

<160> 36

<170> PatentIn version 3.1

<210> 1

<211> 2890

<212> DNA

<213> Bombyx mori

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<221> CDS

<222> (125).. (961)

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aaaa atg aac aat gca gat tta tac cgc aaa agt aac agc ctc caa aag 169

Met Asn Asn Ala Asp Leu Tyr Arg Lys Ser Asn Ser Leu Gln Lys

1 5 10 15

aga gat gct ctg cgc tgc ctc gag gaa cat gcg aat aag att aag tgg 217

Arg Asp Ala Leu Arg Cys Leu Glu Glu His Ala Asn Lys Ile Lys Trp

20 25 30

aaa aaa atc ggt gat aga gtc ata gat ttg ggt tgc gct gac ggt agt 265

Lys Lys Ile Gly Asp Arg Val Ile Asp Leu Gly Cys Ala Asp Gly Ser

35 40 45

gtt act gat att ttg aaa gtt tac atg cca aaa aat tac gga aga tta 313

Val Thr Asp Ile Leu Lys Val Tyr Met Pro Lys Asn Tyr Gly Arg Leu

50 55 60

gtt ggc tgc gac ata agc gaa gaa atg gtg aaa tac gcg aat aaa cac 361

Val Gly Cys Asp Ile Ser Glu Glu Met Val Lys Tyr Ala Asn Lys His

65 70 75

cac ggc ttc ggt agg act tcg ttc agg gtg ctc gac ata gag ggc gat 409

His Gly Phe Gly Arg Thr Ser Phe Arg Val Leu Asp Ile Glu Gly Asp

80 85 90 95

ttg acc gca gac ctg aaa caa ggc ttt gat cac gtt ttc tct ttt tac 457

Leu Thr Ala Asp Leu Lys Gln Gly Phe Asp His Val Phe Ser Phe Tyr

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acc ctc cac tgg atc aga gac cag gaa cga gct ttc cgg aac att ttc 505

Thr Leu His Trp Ile Arg Asp Gln Glu Arg Ala Phe Arg Asn Ile Phe

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Asn Leu Leu Gly Asp Glu Gly Asp Cys Leu Leu Leu Phe Leu Gly His

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act cct atc ttt gat gtt tac cgc aca ctc tcg cat aca gaa aaa tgg 601

Thr Pro Ile Phe Asp Val Tyr Arg Thr Leu Ser His Thr Glu Lys Trp

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cat tct tgg ctc gag cac gtc gat cga ttt ata tca cct tac cat gac 649

His Ser Trp Leu Glu His Val Asp Arg Phe Ile Ser Pro Tyr His Asp

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aat gaa gat ccc gaa aaa gaa gtt aag aag ata atg gaa aga gtt gga 697

Asn Glu Asp Pro Glu Lys Glu Val Lys Lys Ile Met Glu Arg Val Gly

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Phe Ser Asn Ile Glu Val Gln Cys Lys Thr Leu Phe Tyr Val Tyr Asp

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Asp Leu Asp Val Leu Lys Lys Ser Val Ala Ala Ile Asn Pro Phe Asn			
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atc ccg aaa gac ata ctt gaa gac ttt tta gaa gat tac ata gat gta			841
Ile Pro Lys Asp Ile Leu Glu Asp Phe Leu Glu Asp Tyr Ile Asp Val			
225	230	235	
gta cgg gag atg agg ctg ctc gac agg tgt aat aac aat gtc ggt gaa			889
Val Arg Glu Met Arg Leu Leu Asp Arg Cys Asn Asn Asn Val Gly Glu			
240	245	250	255
tca gtg tct ata aaa ttt aac tac aaa gtc atc agt gtt tac gcg aga			937
Ser Val Ser Ile Lys Phe Asn Tyr Lys Val Ile Ser Val Tyr Ala Arg			
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Lys Leu Cys Leu Ser Leu Met			
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Lys Ile Gly Asp Arg Val Ile Asp Leu Gly Cys Ala Asp Gly Ser Val

35 40 45

Thr Asp Ile Leu Lys Val Tyr Met Pro Lys Asn Tyr Gly Arg Leu Val

50 55 60

Gly Cys Asp Ile Ser Glu Glu Met Val Lys Tyr Ala Asn Lys His His
 65 70 75 80

Gly Phe Gly Arg Thr Ser Phe Arg Val Leu Asp Ile Glu Gly Asp Leu
 85 90 95

Thr Ala Asp Leu Lys Gln Gly Phe Asp His Val Phe Ser Phe Tyr Thr
 100 105 110

Leu His Trp Ile Arg Asp Gln Glu Arg Ala Phe Arg Asn Ile Phe Asn
 115 120 125

Leu Leu Gly Asp Glu Gly Asp Cys Leu Leu Leu Phe Leu Gly His Thr
 130 135 140

Pro Ile Phe Asp Val Tyr Arg Thr Leu Ser His Thr Glu Lys Trp His
 145 150 155 160

Ser Trp Leu Glu His Val Asp Arg Phe Ile Ser Pro Tyr His Asp Asn
 165 170 175

Glu Asp Pro Glu Lys Glu Val Lys Lys Ile Met Glu Arg Val Gly Phe
 180 185 190

Ser Asn Ile Glu Val Gln Cys Lys Thr Leu Phe Tyr Val Tyr Asp Asp

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195

200

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Leu Asp Val Leu Lys Lys Ser Val Ala Ala Ile Asn Pro Phe Asn Ile

210

215

220

Pro Lys Asp Ile Leu Glu Asp Phe Leu Glu Asp Tyr Ile Asp Val Val

225

230

235

240

Arg Glu Met Arg Leu Leu Asp Arg Cys Asn Asn Asn Val Gly Glu Ser

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Leu Cys Leu Ser Leu Met

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<222> (1).. (894)

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Asp Ala Lys Leu Ile Leu Asp Glu Phe Ala Ser Thr Met Gln Trp Arg

20 25 30

tcc gat gga gag gat gcc ctc ctg gat gtg ggt tca gga tct ggt aac 144

Ser Asp Gly Glu Asp Ala Leu Leu Asp Val Gly Ser Gly Ser Gly Asn

35 40 45

gtg ctc atg gac ttt gta aag cca ctg ctc ccg att cgt gga caa ctg 192

Val Leu Met Asp Phe Val Lys Pro Leu Leu Pro Ile Arg Gly Gln Leu

50 55 60

gtg ggc aca gac atc tcc agc cag atg gtg cac tat gcc agt aag cat 240

Val Gly Thr Asp Ile Ser Ser Gln Met Val His Tyr Ala Ser Lys His

65 70 75 80

tac cag cga gag gag cgt acc aga ttc cag gtt ctg gac att gga tgc 288

Tyr Gln Arg Glu Glu Arg Thr Arg Phe Gln Val Leu Asp Ile Gly Cys

85 90 95

gaa cgg ctg ccc gag gag ctg agc ggc aga ttt gac cat gtc acc tcg	336
Glu Arg Leu Pro Glu Glu Leu Ser Gly Arg Phe Asp His Val Thr Ser	
100 105 110	
ttc tac tgc ctc cat tgg gtg caa aat ctg aaa gga gct ctc gga aat	384
Phe Tyr Cys Leu His Trp Val Gln Asn Leu Lys Gly Ala Leu Gly Asn	
115 120 125	
atc tac aat ctt ctg aag ccc gaa ggt ggc gac tgc ctc ctg gca ttt	432
Ile Tyr Asn Leu Leu Lys Pro Glu Gly Gly Asp Cys Leu Leu Ala Phe	
130 135 140	
ttg gcc tcc aat ccg gtt tac gaa gtc tat aag att ctt aaa acg aat	480
Leu Ala Ser Asn Pro Val Tyr Glu Val Tyr Lys Ile Leu Lys Thr Asn	
145 150 155 160	
gac aag tgg tcg act tat atg cag gat gtg gag aac ttc ata tcc cca	528
Asp Lys Trp Ser Thr Tyr Met Gln Asp Val Glu Asn Phe Ile Ser Pro	
165 170 175	
ctt cac tac agt cta aat cct ggc gag gaa ttc agc cag ttg ttg aac	576
Leu His Tyr Ser Leu Asn Pro Gly Glu Glu Phe Ser Gln Leu Leu Asn	
180 185 190	
gat gtg ggt ttc gtg caa cac aat gtg gaa att cga aac gaa gtg ttt	624

Asp Val Gly Phe Val Gln His Asn Val Glu Ile Arg Asn Glu Val Phe

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gtt tat gaa ggt gta agg act ctg aaa gat aat gta aag gcc att tgt 672

Val Tyr Glu Gly Val Arg Thr Leu Lys Asp Asn Val Lys Ala Ile Cys

210

215

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cct ttt ctt gag cga atg cct gca gat ttg cat gaa cag ttc ctg gat 720

Pro Phe Leu Glu Arg Met Pro Ala Asp Leu His Glu Gln Phe Leu Asp

225

230

235

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gac ttc ata gac att gtt ata tcc atg aat ttg cag caa ggt gaa aat 768

Asp Phe Ile Asp Ile Val Ile Ser Met Asn Leu Gln Gln Gly Glu Asn

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255

aat gag gat caa aag ttc cta tct ccc tat aaa ctg gtg gtg gcc tat 816

Asn Glu Asp Gln Lys Phe Leu Ser Pro Tyr Lys Leu Val Val Ala Tyr

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265

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gct cgc aag act cct gaa ttt gtg aat aat gtt ttc ctg gag cct aca 864

Ala Arg Lys Thr Pro Glu Phe Val Asn Asn Val Phe Leu Glu Pro Thr

275

280

285

cat caa aac ttg gtt aag gga ata aat taa ttttatttta caaattaaca 914

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Ser Asp Gly Glu Asp Ala Leu Leu Asp Val Gly Ser Gly Ser Gly Asn

35 40 45

Val Leu Met Asp Phe Val Lys Pro Leu Leu Pro Ile Arg Gly Gln Leu

50 55 60

Val Gly Thr Asp Ile Ser Ser Gln Met Val His Tyr Ala Ser Lys His

65 70 75 80

Tyr Gln Arg Glu Glu Arg Thr Arg Phe Gln Val Leu Asp Ile Gly Cys

1 4 / 4 9

85

90

95

Glu Arg Leu Pro Glu Glu Leu Ser Gly Arg Phe Asp His Val Thr Ser

100

105

110

Phe Tyr Cys Leu His Trp Val Gln Asn Leu Lys Gly Ala Leu Gly Asn

115

120

125

Ile Tyr Asn Leu Leu Lys Pro Glu Gly Gly Asp Cys Leu Leu Ala Phe

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135

140

Leu Ala Ser Asn Pro Val Tyr Glu Val Tyr Lys Ile Leu Lys Thr Asn

145

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155

160

Asp Lys Trp Ser Thr Tyr Met Gln Asp Val Glu Asn Phe Ile Ser Pro

165

170

175

Leu His Tyr Ser Leu Asn Pro Gly Glu Glu Phe Ser Gln Leu Leu Asn

180

185

190

Asp Val Gly Phe Val Gln His Asn Val Glu Ile Arg Asn Glu Val Phe

195

200

205

Val Tyr Glu Gly Val Arg Thr Leu Lys Asp Asn Val Lys Ala Ile Cys

210

215

220

1 5 / 4 9

Pro Phe Leu Glu Arg Met Pro Ala Asp Leu His Glu Gln Phe Leu Asp

225

230

235

240

Asp Phe Ile Asp Ile Val Ile Ser Met Asn Leu Gln Gln Gly Glu Asn

245

250

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Asn Glu Asp Gln Lys Phe Leu Ser Pro Tyr Lys Leu Val Val Ala Tyr

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<213> *Anopheles gambiae*

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<222> (1).. (855)

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gat gcg atg gag ata ttg aaa gaa tac gca cca ctc atc agc tgt cca 96

Asp Ala Met Glu Ile Leu Lys Glu Tyr Ala Pro Leu Ile Ser Cys Pro

20 25 30

agg gat ggc gaa gag gtt gcc ctg tta gac att ggg tgt ggc agc ggg 144

Arg Asp Gly Glu Glu Val Ala Leu Leu Asp Ile Gly Cys Gly Ser Gly

35 40 45

gac gtg ttg gtg gac tac att cta ccg gtg ctg agc cgc gga agc act 192

Asp Val Leu Val Asp Tyr Ile Leu Pro Val Leu Ser Arg Gly Ser Thr

50 55 60

cct gtg gcg cgc gca ttg gcg aca gac atc tcg gag cag atg gtg cgc 240

Pro Val Ala Arg Ala Leu Ala Thr Asp Ile Ser Glu Gln Met Val Arg

65 70 75 80

cat gca cgt gaa tcg tac cgt cac gtt aag acg atc gag ttc gac acc 288

His Ala Arg Glu Ser Tyr Arg His Val Lys Thr Ile Glu Phe Asp Thr

85 90 95

ctt gac atc ggc atc aaa ctc gat agt gca aag ttg tcc cgc tgg gga 336

Leu Asp Ile Gly Ile Lys Leu Asp Ser Ala Lys Leu Ser Arg Trp Gly

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105

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Gln Phe Ser His Val Thr Ser Phe Tyr Cys Leu His Trp Val Gln Asn

115

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cag cac gta gcc ttt tcc aac atc tac aac ctt ctg cag cat ggc ggt 432

Gln His Val Ala Phe Ser Asn Ile Tyr Asn Leu Leu Gln His Gly Gly

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aac caa ctg tct cgc tca ccc aag tgg tcc aag tat atg tac gac gtg 528

Asn Gln Leu Ser Arg Ser Pro Lys Trp Ser Lys Tyr Met Tyr Asp Val

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gaa aag tac att tcg ccc tac cag tat tgt gaa aat cca gca agt gag 576

Glu Lys Tyr Ile Ser Pro Tyr Gln Tyr Cys Glu Asn Pro Ala Ser Glu

180

185

190

atc gag gat ctg ctg tgc acg gtg ggc ttt cag cag tat cag ata cag 624

Ile Glu Asp Leu Leu Cys Thr Val Gly Phe Gln Gln Tyr Gln Ile Gln

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Val Arg Asp Lys Leu Tyr Val Tyr Glu Gly Leu Asp Asn Leu Lys Arg

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215

220

gca gtt ttg gct gtg aat cca ttc agt gaa cga atg cca cca gaa ctg 720

Ala Val Leu Ala Val Asn Pro Phe Ser Glu Arg Met Pro Pro Glu Leu

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230

235

240

cag gat agg ttc cta ctg gac tat atc gct gtt gtg cgg cag atg tac 768

Gln Asp Arg Phe Leu Leu Asp Tyr Ile Ala Val Val Arg Gln Met Tyr

245

250

255

ttg acc aaa act ggc agc gaa gag aat gat tgc aat ctt caa ttc ata 816

Leu Thr Lys Thr Gly Ser Glu Glu Asn Asp Cys Asn Leu Gln Phe Ile

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tcc cca tac aag ttg gtg gtt gtt tat gcg aag aaa taa 855

Ser Pro Tyr Lys Leu Val Val Val Tyr Ala Lys Lys

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<400> 6

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Arg Asp Gly Glu Glu Val Ala Leu Leu Asp Ile Gly Cys Gly Ser Gly

35 40 45

Asp Val Leu Val Asp Tyr Ile Leu Pro Val Leu Ser Arg Gly Ser Thr

50 55 60

Pro Val Ala Arg Ala Leu Ala Thr Asp Ile Ser Glu Gln Met Val Arg

65 70 75 80

His Ala Arg Glu Ser Tyr Arg His Val Lys Thr Ile Glu Phe Asp Thr

85 90 95

Leu Asp Ile Gly Ile Lys Leu Asp Ser Ala Lys Leu Ser Arg Trp Gly

100 105 110

Gln Phe Ser His Val Thr Ser Phe Tyr Cys Leu His Trp Val Gln Asn

115 120 125

20 / 49

Gln His Val Ala Phe Ser Asn Ile Tyr Asn Leu Leu Gln His Gly Gly

130

135

140

Asp Cys Leu Leu Val Phe Leu Ala Asn Asn Pro Ile Phe Asp Ile Tyr

145

150

155

160

Asn Gln Leu Ser Arg Ser Pro Lys Trp Ser Lys Tyr Met Tyr Asp Val

165

170

175

Glu Lys Tyr Ile Ser Pro Tyr Gln Tyr Cys Glu Asn Pro Ala Ser Glu

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Ile Glu Asp Leu Leu Cys Thr Val Gly Phe Gln Gln Tyr Gln Ile Gln

195

200

205

Val Arg Asp Lys Leu Tyr Val Tyr Glu Gly Leu Asp Asn Leu Lys Arg

210

215

220

Ala Val Leu Ala Val Asn Pro Phe Ser Glu Arg Met Pro Pro Glu Leu

225

230

235

240

Gln Asp Arg Phe Leu Leu Asp Tyr Ile Ala Val Val Arg Gln Met Tyr

245

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Leu Thr Lys Thr Gly Ser Glu Glu Asn Asp Cys Asn Leu Gln Phe Ile

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<222> (111)..(932)

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Met Asn

1

aac gcc gtt ttg tac gaa caa gct aac agc atg cag aag aga gat gca 164

Asn Ala Val Leu Tyr Glu Gln Ala Asn Ser Met Gln Lys Arg Asp Ala

5

10

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ctc aac ttt tta gac gac atc tcc cct aaa cta aag tgg aag aag agt 212

Leu Asn Phe Leu Asp Asp Ile Ser Pro Lys Leu Lys Trp Lys Lys Ser

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25

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atc agc aac att ctg gac gta gga tgt gga gat gga tgt gtc acc agc 260

Ile Ser Asn Ile Leu Asp Val Gly Cys Gly Asp Gly Cys Val Thr Ser

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atg ctt aaa aag tac atc cct act gac ttc aag ctg ctc ggc tgt gac 308

Met Leu Lys Lys Tyr Ile Pro Thr Asp Phe Lys Leu Leu Gly Cys Asp

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atc agt gag aag atg gtg aat ttc gcc aat gac cac cat tgc aat gaa 356

Ile Ser Glu Lys Met Val Asn Phe Ala Asn Asp His His Cys Asn Glu

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cag acg tcg ttc aca gtg ctg gac atc gca gga gat ata ccc gaa ggt 404

Gln Thr Ser Phe Thr Val Leu Asp Ile Ala Gly Asp Ile Pro Glu Gly

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atg aag gga aaa ttc gac cat gtt ttc tcc ttc tat gcc ttg cac tgg 452

Met Lys Gly Lys Phe Asp His Val Phe Ser Phe Tyr Ala Leu His Trp

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105

110

gtc ttg gat caa gag cgc gta ttc agg aat att tac gat ttg ctg agt 500

Val Leu Asp Gln Glu Arg Val Phe Arg Asn Ile Tyr Asp Leu Leu Ser

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Lys Asp Gly Glu Cys Phe Thr Ile Phe Val Ala Gly Ala Pro Val Phe				
	135	140	145	
gac ttg tac cgc att tta tcg cgt aac aac aaa tgg agc act ctg ctt				596
Asp Leu Tyr Arg Ile Leu Ser Arg Asn Asn Lys Trp Ser Thr Leu Leu				
	150	155	160	
aaa gat gtc gag aaa tac ata tcg cca tac cac gac tca cag gat cca				644
Lys Asp Val Glu Lys Tyr Ile Ser Pro Tyr His Asp Ser Gln Asp Pro				
	165	170	175	
gcg aaa gaa atg aga aaa gta ttg gaa aaa gtt gga tac gtg gac tac				692
Ala Lys Glu Met Arg Lys Val Leu Glu Lys Val Gly Tyr Val Asp Tyr				
	180	185	190	
aag gtg gaa tgt aaa aac ttg gtg tat atg tac aac aac ttc gcc agt				740
Lys Val Glu Cys Lys Asn Leu Val Tyr Met Tyr Asn Asn Phe Ala Ser				
195	200	205	210	
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Leu Trp Lys Thr Leu Gln Ala Ile Asn Pro Phe Asn Ile Pro Lys Asp				
	215	220	225	

24 / 49

atg gaa gaa gat ttc aaa caa gat tac tta aat att tta aaa gat atg 836

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230

235

240

aaa att gtg tct aag tat aat acc gat gag gca agt gtg aac ttc aaa 884

Lys Ile Val Ser Lys Tyr Asn Thr Asp Glu Ala Ser Val Asn Phe Lys

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250

255

tat cgg ttg ctt gtc gta cac gct cgc aag ccg gcc tca gaa ttt tag 932

Tyr Arg Leu Leu Val Val His Ala Arg Lys Pro Ala Ser Glu Phe

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ggaaaataat cacaaataaa ctaactgaat atttgtagta caataacaaa acctgatgca 992

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<211> 273

<212> PRT

<213> Spodoptera litura

<400> 8

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15

25 / 49

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25

30

Lys Ser Ile Ser Asn Ile Leu Asp Val Gly Cys Gly Asp Gly Cys Val

35

40

45

Thr Ser Met Leu Lys Lys Tyr Ile Pro Thr Asp Phe Lys Leu Leu Gly

50

55

60

Cys Asp Ile Ser Glu Lys Met Val Asn Phe Ala Asn Asp His His Cys

65

70

75

80

Asn Glu Gln Thr Ser Phe Thr Val Leu Asp Ile Ala Gly Asp Ile Pro

85

90

95

Glu Gly Met Lys Gly Lys Phe Asp His Val Phe Ser Phe Tyr Ala Leu

100

105

110

His Trp Val Leu Asp Gln Glu Arg Val Phe Arg Asn Ile Tyr Asp Leu

115

120

125

Leu Ser Lys Asp Gly Glu Cys Phe Thr Ile Phe Val Ala Gly Ala Pro

130

135

140

Val Phe Asp Leu Tyr Arg Ile Leu Ser Arg Asn Asn Lys Trp Ser Thr

145

150

155

160

26 / 49

Leu Leu Lys Asp Val Glu Lys Tyr Ile Ser Pro Tyr His Asp Ser Gln

165

170

175

Asp Pro Ala Lys Glu Met Arg Lys Val Leu Glu Lys Val Gly Tyr Val

180

185

190

Asp Tyr Lys Val Glu Cys Lys Asn Leu Val Tyr Met Tyr Asn Asn Phe

195

200

205

Ala Ser Leu Trp Lys Thr Leu Gln Ala Ile Asn Pro Phe Asn Ile Pro

210

215

220

Lys Asp Met Glu Glu Asp Phe Lys Gln Asp Tyr Leu Asn Ile Leu Lys

225

230

235

240

Asp Met Lys Ile Val Ser Lys Tyr Asn Thr Asp Glu Ala Ser Val Asn

245

250

255

Phe Lys Tyr Arg Leu Leu Val Val His Ala Arg Lys Pro Ala Ser Glu

260

265

270

Phe

<211> 1193

<212> DNA

<213> *Helicoverpa armigera*

<220>

<221> CDS

<222> (124).. (978)

<223>

<400> 9

actgtccgcc gaaaccgcgc ttcaactcaac cacgcgcacg cgcacccgaa aataaataac 60

aagaatcata aactaaacaa atcaatatca cgaaattcaa atacctataa aaaaatcctt 120

aaa atg aat aac gcg gtc ttg tat gaa aaa agc aat agc ttg cag aag 168

Met Asn Asn Ala Val Leu Tyr Glu Lys Ser Asn Ser Leu Gln Lys

1 5 10 15

aga gat gct atc atg tgt cta gaa gaa tac gct tcg aaa att aag tgg 216

Arg Asp Ala Ile Met Cys Leu Glu Glu Tyr Ala Ser Lys Ile Lys Trp

20 25 30

aag aag agt aat aat aat att ctt gac ata ggc tgt ggg gat gga agc 264

Lys Lys Ser Asn Asn Asn Ile Leu Asp Ile Gly Cys Gly Asp Gly Ser

35 40 45

gtg act aat atg ctg aag aaa tac atc cct act gag tac aag ttg ctt	312
Val Thr Asn Met Leu Lys Lys Tyr Ile Pro Thr Glu Tyr Lys Leu Leu	
50 55 60	
ggc tgt gat att agc gag aag atg gtg aac ttc gcg aat gat cat cat	360
Gly Cys Asp Ile Ser Glu Lys Met Val Asn Phe Ala Asn Asp His His	
65 70 75	
tgt aac gaa cag act tct ttc acc gtg ctc gat att gag gga gac cta	408
Cys Asn Glu Gln Thr Ser Phe Thr Val Leu Asp Ile Glu Gly Asp Leu	
80 85 90 95	
cct gaa ggt atg aag gga aac ttc gac cac gtt ttc tcg ttc tac gct	456
Pro Glu Gly Met Lys Gly Asn Phe Asp His Val Phe Ser Phe Tyr Ala	
100 105 110	
ctg cac tgg gtt aat aac caa gaa cga gca ttc aaa aac ata tac aac	504
Leu His Trp Val Asn Asn Gln Glu Arg Ala Phe Lys Asn Ile Tyr Asn	
115 120 125	
ctt cta agc gag gat ggg gag tgc ttc acg ata ttc gta gcc tgg gct	552
Leu Leu Ser Glu Asp Gly Glu Cys Phe Thr Ile Phe Val Ala Trp Ala	
130 135 140	
cct gtg ttt gac gtg tac cga gtg ctc gcg cgc aac aac aag tgg agt	600
Pro Val Phe Asp Val Tyr Arg Val Leu Ala Arg Asn Asn Lys Trp Ser	

145	150	155	
caa tgg gtg cat gat gtc gac aga tac ata tcg ccc tac cac gac tct			648
Gln Trp Val His Asp Val Asp Arg Tyr Ile Ser Pro Tyr His Asp Ser			
160	165	170	175
ttg gag ccg gaa aaa gat tta aag gct atg ata gac aaa att gga ttc			696
Leu Glu Pro Glu Lys Asp Leu Lys Ala Met Ile Asp Lys Ile Gly Phe			
	180	185	190
gtt gac atc gat gtg gaa tgt aaa gaa ttg gta ttc gtg tac gac aac			744
Val Asp Ile Asp Val Glu Cys Lys Glu Leu Val Phe Val Tyr Asp Asn			
	195	200	205
ata cat att ttg cga aaa gcg tta aca gca atc aac cct ttc aaa atc			792
Ile His Ile Leu Arg Lys Ala Leu Thr Ala Ile Asn Pro Phe Lys Ile			
	210	215	220
ccc aag gaa aaa tat gat gat ttc atg gaa gac tat atg gat ata ctg			840
Pro Lys Glu Lys Tyr Asp Asp Phe Met Glu Asp Tyr Met Asp Ile Leu			
	225	230	235
aaa gaa cta caa att tta gac aag tac aac aat aat tat gaa aag agc			888
Lys Glu Leu Gln Ile Leu Asp Lys Tyr Asn Asn Asn Tyr Glu Lys Ser			
240	245	250	255

gtt gaa ttc aat tac cgt ttg ctt gta gtg tat gcc cga aaa cct gac 936

Val Glu Phe Asn Tyr Arg Leu Leu Val Val Tyr Ala Arg Lys Pro Asp

260

265

270

tcg cag gat aaa atg tta gaa gct cta aat gga caa acg tag 978

Ser Gln Asp Lys Met Leu Glu Ala Leu Asn Gly Gln Thr

275

280

actgaaaaac ttatatTTTT agttacggca aaatacagtg tagaacagtt atttgtagtt 1038

aaggatgaat gtatagtgtat tctcttcagg tttagttttg ggcctgggtat gaaatgttgt 1098

ttttttaagt aagctatTTTT ggtaatgtaa actatTTTTa aaggcaggaa aataatctgt 1158

gtgtgagcaa aaaaaaaaaa aaaaaaaaaa aaaaa 1193

<210> 10

<211> 284

<212> PRT

<213> Helicoverpa armigera

<400> 10

Met Asn Asn Ala Val Leu Tyr Glu Lys Ser Asn Ser Leu Gln Lys Arg

1

5

10

15

3 1 / 4 9

Asp Ala Ile Met Cys Leu Glu Glu Tyr Ala Ser Lys Ile Lys Trp Lys

20

25

30

Lys Ser Asn Asn Asn Ile Leu Asp Ile Gly Cys Gly Asp Gly Ser Val

35

40

45

Thr Asn Met Leu Lys Lys Tyr Ile Pro Thr Glu Tyr Lys Leu Leu Gly

50

55

60

Cys Asp Ile Ser Glu Lys Met Val Asn Phe Ala Asn Asp His His Cys

65

70

75

80

Asn Glu Gln Thr Ser Phe Thr Val Leu Asp Ile Glu Gly Asp Leu Pro

85

90

95

Glu Gly Met Lys Gly Asn Phe Asp His Val Phe Ser Phe Tyr Ala Leu

100

105

110

His Trp Val Asn Asn Gln Glu Arg Ala Phe Lys Asn Ile Tyr Asn Leu

115

120

125

Leu Ser Glu Asp Gly Glu Cys Phe Thr Ile Phe Val Ala Trp Ala Pro

130

135

140

Val Phe Asp Val Tyr Arg Val Leu Ala Arg Asn Asn Lys Trp Ser Gln

145

150

155

160

Trp Val His Asp Val Asp Arg Tyr Ile Ser Pro Tyr His Asp Ser Leu

165

170

175

Glu Pro Glu Lys Asp Leu Lys Ala Met Ile Asp Lys Ile Gly Phe Val

180

185

190

Asp Ile Asp Val Glu Cys Lys Glu Leu Val Phe Val Tyr Asp Asn Ile

195

200

205

His Ile Leu Arg Lys Ala Leu Thr Ala Ile Asn Pro Phe Lys Ile Pro

210

215

220

Lys Glu Lys Tyr Asp Asp Phe Met Glu Asp Tyr Met Asp Ile Leu Lys

225

230

235

240

Glu Leu Gln Ile Leu Asp Lys Tyr Asn Asn Asn Tyr Glu Lys Ser Val

245

250

255

Glu Phe Asn Tyr Arg Leu Leu Val Val Tyr Ala Arg Lys Pro Asp Ser

260

265

270

Gln Asp Lys Met Leu Glu Ala Leu Asn Gly Gln Thr

275

280

<210> 11

<211> 17

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 11

tttttttttt tttttgc

17

<210> 12

<211> 10

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 12

gatcatagcc

10

<210> 13

<211> 25

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 13

aagccgcagt aagatggcgg tggtg

25

<210> 14

<211> 25

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 14

caacaccgcc atcttactgc ggctt

25

<210> 15

<211> 30

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 15

aaacatatga acaatgcaga tttataccgc

30

<210> 16

<211> 30

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 16

aaggatccaa tcacgaaaat ctgggaagac

30

<210> 17

<211> 30

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 17

aaacatatga atcaggcctc tctatatcag

30

<210> 18

<211> 34

<212> DNA

<213> Artificial

<220>

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<400> 18

aaggatccga ctctgttaac aaatgcaatt actg

34

<210> 19

<211> 23

<212> DNA

<213> Artificial

<220>

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<221> misc_feature

<222> (6).. (6)

<223> "n"=A, T, G or C

<220>

<221> misc_feature

<222> (15).. (15)

<223> "n"=A, T, G or C

<400> 19

atggtnaart aygcnaayaa rca

23

<210> 20

<211> 23

<212> DNA

<213> Artificial

<220>

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<220>

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<222> (6).. (6)

<223> "n"=A, T, G or C

<220>

<221> misc_feature

<222> (12).. (12)

<223> "n"=A, T, G or C

<400> 20

taraangara anacrtgrtc raa

23

<210> 21

<211> 28

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 21

ttcacagtgc tggacatcgc aggagata

28

<210> 22

<211> 28

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 22

tatctcctgc gatgtccagc actgtgaa

28

<210> 23

<211> 26

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 23

cgaacagact tctttcaccg tgctcg

26

<210> 24

<211> 26

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 24

cgagcacggt gaaagaagtc tgttcg

26

<210> 25

<211> 30

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 25

aaacatatga ataacgccgt tttgtacgaa

30

<210> 26

<211> 30

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 26

aactcgagct tgcatacaggt ttgtttattg

30

<210> 27

<211> 30

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 27

aaacatatga ataacgcggt cttgtatgaa

30

<210> 28

<211> 30

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 28

aactcgaggc ccaaaactaa acctgaagag

30

<210> 29

<211> 8

<212> PRT

<213> Artificial

<220>

<223> consensus sequence

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<222> (2).. (2)

<223> "Xaa"=Asp or Glu

<220>

<221> MISC_FEATURE

<222> (3).. (3)

<223> "Xaa"=hydrophobic amino acid

<220>

<221> MISC_FEATURE

<222> (5).. (5)

<223> "Xaa"=low molecular weight neutral amino acid

<220>

<221> MISC_FEATURE

<222> (7).. (7)

<223> "Xaa"=low molecular weight neutral amino acid

<400> 29

Leu Xaa Xaa Gly Xaa Gly Xaa Gly

1

5

<210> 30

<211> 18

<212> PRT

<213> Artificial

<220>

<223> consensus sequence

<220>

<221> MISC_FEATURE

<222> (5).. (5)

<223> "Xaa"=any amino acid

<220>

<221> MISC_FEATURE

<222> (8).. (8)

<223> "Xaa"=Gln or Glu

<220>

<221> MISC_FEATURE

<222> (9).. (9)

<223> "Xaa"=His, Lys or Gln

<220>

<221> MISC_FEATURE

<222> (13).. (13)

<223> "Xaa"=hydrophobic amino acid

<400> 30

Met Asn Asn Ala Xaa Leu Tyr Xaa Xaa Ala Asn Ser Xaa Gln Lys Arg

1 5 10 15

Asp Ala

<210> 31

<211> 9

<212> PRT

<213> Artificial

<220>

<223> consensus sequence

<220>

<221> MISC_FEATURE

<222> (1).. (1)

<223> "Xaa"=Leu, Val or Ile

<220>

<221> MISC_FEATURE

<222> (4).. (4)

<223> "Xaa"=Leu, Val or Ile

<400> 31

Xaa Leu Asp Xaa Gly Cys Gly Asp Gly

1

5

<210> 32

<211> 12

<212> PRT

<213> Artificial

<220>

<223> consensus sequence

<220>

<221> MISC_FEATURE

<222> (1).. (1)

<223> "Xaa"=Gln, Arg or Lys

<220>

<221> MISC_FEATURE

<222> (3).. (3)

<223> "Xaa"=Leu or Val

<220>

<221> MISC_FEATURE

<222> (10).. (10)

<223> "Xaa"=Gln or Lys

<400> 32

Xaa Leu Xaa Gly Cys Asp Ile Ser Glu Xaa Met Val

1

5

10

<210> 33

<211> 13

<212> PRT

<213> Artificial

<220>

<223> consensus sequence

<220>

<221> MISC_FEATURE

<222> (9).. (9)

<223> "Xaa"=Cys, Thr or Ala

<400> 33

Phe Asp His Val Phe Ser Phe Tyr Xaa Leu His Trp Val

1

5

10

<210> 34

<211> 9

<212> PRT

<213> Artificial

<220>

<223> consensus sequence

<220>

<221> MISC_FEATURE

<222> (2).. (2)

<223> "Xaa"=Val or Ile

<220>

<221> MISC_FEATURE

<222> (5).. (5)

<223> "Xaa"=Val, Ile or Leu

<220>

<221> MISC_FEATURE

<222> (8).. (8)

<223> "Xaa"=Ile or Val

<400> 34

Pro Xaa Phe Asp Xaa Tyr Arg Xaa Leu

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5

<210> 35

<211> 12

<212> PRT

<213> Artificial

<220>

<223> consensus sequence

<220>

<221> MISC_FEATURE

<222> (4).. (4)

<223> "Xaa"=Lys or Arg

<400> 35

49 / 49

Asp Val Glu Xaa Tyr Ile Ser Pro Tyr His Asp Ser

1 5 10

<210> 36

<211> 10

<212> PRT

<213> Artificial

<220>

<223> consensus sequence

<220>

<221> MISC_FEATURE

<222> (4).. (4)

<223> "Xaa"=Ile, Val or Leu

<400> 36

Tyr Lys Leu Xaa Val Val Tyr Ala Arg Lys

1 5 10